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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Frequentity
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OM protein - protein search, using sw model

Prin on:

(without alignments) 58.517 Million cell updates/sec Tabuary 16, 2003, 16 42 17 , Search time 18 0714 Seconds

45-04-856-070-23

1 ELMLPLODYEE 11 Perfect score. Sednence:

Gapop 10.0 , Gapext 0.5 RI OSIIM62 Scoring table:

283224 seqs, 96134422 residues Searched: Fotal number of hits satisfying chosen parameters.

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pir1:* PIR_73:*

pir2:* pir3.* pir4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

		æ					
Result		Query					
No.	Score	Match	Length	BB	ID	Descri	Description
_	55	100.0	581	7	145889	Czrin	- bovine
2	55	100 0	586		A 34400	ezrin	[validated]
m	55		630	C4	T47177	hypoth	hypothetical prote
4	n C1	94.5	586		B41129	ezrin	- mouse
S	38	69.1	130	CI	H84133	hypoth	hypothetical prote
œ	38	69.1	150	C1	C97449	hypoth	hypothetical trans
7	38	69.1	150	C÷	AP2667	trans.	transpription regu
30	3.7	67.3	 	CI	112857	hypoth	Eypothetical profe
n	37	67.3	321	C 1	H82832	protei	-
10	7.7	67 3	23.5	_	A70364	1980CO	conserved hypothet
11	3.7	7	1058	7	S65460	apolip	polipoprotein B -
13	36	5.00	000	<u>(1</u>	A83244	тарион	conserved hypothet
13	36		284	Cı	D84790	probat	probable adenylate
14	36.		grr	CI	tuuč8J	158005	conserved hypothet
15	36	9.0	, u	C a	80108	fodr i:	odrin alpha chain
16	36	65.5	2472	:4	A35715	todrir	odrin alpha chain
17	36		2477	Н	SJCHA	spectrin	rin alpha cha
18	35	63.6	99		A84093	hypoth	hypothetical prote
19	35		۲. د		136984	hypoth	Typothetical prote
20	υ· ~		122	C1	H97242	probable	phos
 			177	C1	T01828	hypoti	hypothetical prote
<u></u>		~	G-08	,	LAHENA	alpha	alpha actinin 1
23	35		964	2	D59404	plectin	in isotorm pl
₹.	u) Ži	£.3 €.3	45.74	C a	U05205	ni toslo	iti publist, iti
52	35	63.6	46.R4	CA	A59404	piertis	in (imported)
26	35	٠.	4687	,	A39638	plectin	. 1
2.7		61.8	105		869333	conscr	conserved hypothet
28	34	Ξ.	250	C 3	1184212	hypoth	hypothetical profe
64	34	α.	\$27	۲.	742999	othan.	othanolamine phosp

61.8 332 2 \$31926 51.8 333 2 \$31098 51.8 333 2 \$31098 61.8 333 2 \$44082 61.8 387 2 \$44082 61.8 405 2 \$34082 61.8 454 2 \$34620 61.8 454 2 \$36661 61.8 510 2 \$70825 61.8 510 2 \$70825	88 88 88 88 88 84 84 88 88 88 88 88 88 8
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ALIGNMENTS

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MAISTERACE TRANSCENTING BENEFICION, VILLIA 2
C.Species, Edua sapiens (man)
C.Species, Edua sapiens (man)
C.Species, 22 Tan 1990 #ragreene_revision 14 Tal 1994 #fext_change 08 Der 2000
C.Accession, S. Waloo, S09258; E51002
F.Turner, C. Waloo, S09258; E51009
F.Turner, C. Waloo, S09258; Parze 1999
A.Title, Cyturilla, a microfilia; Mrr 75,000 protein, COMA Sequence, prokaryotic exp
A.Reference makes, A34400, Multi-2674140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anolecule type: mENA
A.Residues: 1-586 <TURA
A.Cossificatedes. 200321
A.Note. the translation of residues : 11 is not given
A.Note. parts of this sequence were confilmed by protein sequencing
R.Gould, K.L. Bretandher, A.: Esch. F.S.; Hunter, T.
EMBO J. 8. 4133 4442, 1989
A.III.e. cDNA clouded and sequencing of the protein tyroside kinase substrate, ezrin,
A.Keterence number. 303263; MUD199075135; PMID12591371
                                                                                                                                            RyBergson, C.M.; Zhao, H., Saijoh, K.; Duman, R.S.; Nestler, E.J.
Mol. Cell. Neurosci. 4, 64-73, 1993
AyTille: Ezrim and osteomectin, two proteins associated with cell shape and growth, a
AyPeference number: 145889
AyAcession: 145889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ċ
                                                    C.Species: Bos primigenius taurus (cattle)
C.Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 14-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                A)Cross-references: GB:M98498; NID:q289407; FIDN:AAA30510.1; FID:q289408
C)Superlamily: ezrin: profein 4 1 membrane-binding domain homology
F)7-291/Foomain: profein 4.1 membrane-binding domain homology <841>
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100.0%; Pred. No. 0.017;
alive 0, Mishaltches 0, Indeis
                                                                                                                                                                                                                                                                                                        A)Status: preliminary; translated from GH/EMBL/JDDBJ
A)Molecule type: mRNA
A)Residues: 1-581 <HER>
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Best Local Similarity 100.0
Matches II, Conservative
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A,Residues, 2.586 <GOC>
                                                                                                                        C;Accession: 145889
                          - bovine
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145889
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A, Cross references, 38.X51521, NTC-431282, FIDALONASS893.1, PTC.431283

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AJCIOSS IEFELENCES: EMBLINAGET1; NID:9508BU; PIDN:CAA430B6.1; PID:450BH1
EJEGETION, M.; Burgess, W.H.; Chen, D.; Druker, B.J.; Hietscher, A.; Samelson, L.E.
J. Imminol. 149, 1847-1852, 1992
AJTILLE: Identilication of ezrin as an 81-kDa tyrosine-phosphorylated protein in T ee
A.Reterence number: A46501; MUID:92388649; PMID:1381389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RyTakami, H., Nakasone, K., Takaki, Y., Mactio, G.; Sasaki, R.; Masul, N.; Fuji, F.; H. Nucleic Acids for. 28, 4337-2000
Nucleic Acids for. 28, 4337-2000
A.Title. Complete geneine sequence of the alkaliphilic bacterium Racillus halodurans a
A.Feferege malage AR 6550, MTH. 20612582, FMID. 11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Comment: This protein is located in microvilli and is proposed to play a role in mo C:Superfamily. carin, protein 4.1 membrane-binding domain homology
C:Keywords: actin binding: cytoskeleton; cytosol; membrane-associated protein; phosph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Cross-references: GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB07591.1; GSPDH:G
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C;Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Bacillus halodurans
C;Dute: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: H84133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein BH3872 (imported) · Bacillus halodurans (strain 0-125)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :214,299,332/Binding site: phosphate (Thr) (covalent) #status predicted
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F;7-291/Domain: protein 4.1 membrane-binding domain homology -B41>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;66/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.5%; Score 52; DB 1; Length 586;
90.9%; Pred. No. 0.065;
.ive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Molecule type: protein
A.Residues: 53-57,148,127,156,767,152-155 «EG3>
A.Experimental source: MRL lpr/lpr, T-cells
A.Note: sequence extracted from NCBI backbone (NCBIP:112940)
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule, type: protein
A;Residues: 27-33, E' <EG2>
A;Experimental source: MKL lpr/lpr, T-cells
A;Note: sequence extracted from NCBI backbone (NCBIE:112936)
A,Accession: 846501
                                                                                                                                                                                                                                                                                                                                               A; Note: sequence extracted from NCBI backbone (NCBIP:112938)
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                                                                                                                                                                                                                                            ArMolecale type: profein
ArResidues: 412-426 <EGE>
ArExperimental source: MRL lpr/lpr, I-cells
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Matches 10; Conservative
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                                                                                                                                                                                                                A, Status, preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A4650
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                                                                                                                                                           A.Molecule type: protein
A.Residues 255-263:194, Q.,196-199, X.,201,264-270 -BAUA
A.Note: it is not certain whether this material represents errin or radixin (see entry A.Note: this material corresponds to transformed epithelial amnion cell (AMA) database p
C.Comment: This protein is located in microvilli and is proposed to play a role in modul
   Hanw, G., Kasmusson, H.H.; yan ben Hulcke, M.; Van Damme, J., Puype, M., Gesser, H., d
                               Electrophoresis II, 528-536, 1990
A.Title: Two-dimensional gel electrophoresis, protein electroblotting and microsequencin
A.Reference number: A61002; MUID:91031404; PMID.1699755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Superfamily: ezrin: profein 4 1 membrane-binding domain homology
C.Keywords: actin binding; cytoskeleton: membrane associated profein; phosphoprotein
P:2-586/Product: ezrin #status experimental <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ** #sequence_revision 20 Apr 2000 *text_change 02:Sep 2000
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: mkwa
A;Residues: 1-640 <AAA>
A;Cross-references: EMBL:AL162086
A;Cross-references: EMBL:AL162086
C;Genetics:
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Fi214,299,332/Winding site: phosphate (Thr) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ċ
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Pred. No. 0.019;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submittled to the Protein Sequence Database, March 2000
A;Reference number: 224377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein DKF2p762H157.1 human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F12-586,Pproduct: earin #status experimental aMAT>
F17-291,Thomsin: protein 4.1 membrane binding domain
F1553-586/Region: actin binding #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GDB:120489; OMIM:123900
A;Map position: 6q25-6q26
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Date: 20:Apr-2000 #sequence
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446 ELMLRLQDYRE 356
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Matches 11: Conserv
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A:Residues: 1-586 <FUN>
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                                                                                                                                      A; Accession: E61002
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C; Superfamily: Escherichia coli preprotein translocase chain sech
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   A, Residues: 1:111 -LAZ>
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A;Gene: XFC
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Pypotherical protein yopw - Bacillus subtills phage SPB-22

C.Species. Bacillus subtilis phage SPB-2

C.Species. Bacillus subtilis phage SPB-2

C.Date: 13-Aug-1999 *Sequence_revision 13-Aug-1999 *text_change 20-Jsn-2000

C.Accession: T18857. E69918

B.Lazarevic, V. Bussterholt, A.. Schor, B.; Hilbert, H., Manel, C., Karamata, D.

Submitted to the EMBL Data Library, Angust 1997

A.Reforence number: 27583

A.Reforence number: 27583
                                                                                                                                              A:Iftle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobactorium tum
A:Reterence number: A97459; PMID:11743194
A:Status; prefiminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agrobacterium tumefaciens (str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, A.; Karp, P.; Romero, P.; Zhang, S. Science 244, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Ridile, P.; Junq, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                               Rydovddor, M.; Hibble, G.; Sattudy, S.; Miller, N.; Rhanchord, M.; Surello, R., Geldmar
A.; Liu, F.; Wolldm, C.; Allinger, M., Doughty, D., Soutt, C.; Lappas, C., Markelz, R.
Science 291, 2322-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Title: The Derome of the Natural Cenetic Engineer Agrebacterium tumefacions CS8. A,Reference number: AR2577; PMID:11743193
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                                                                                                                                                                                                                                                                                                                                  A)Cross-references: GB:AE007869; PIDN:AAK86548 1, PID q19155710, 3SPDB 3N60169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcription regulator, AsiC family Ata0740 (imported). Agrobacterium tume
CiSpecies: Agrobacterium tumelaciens
CiDate: 11-Tan-võid rsequence_revision 11-Tan-võid riext_change ~1 Feb 2002
CiAccession: AF2667
C)Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
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Fred. No. 6.7,
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A,Molecule type: DNA
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1; Mismatches
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80.0%; Pred. No.
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C:Superfamily: regulatory protein asnC
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: circular chromosome
C:Superfamily: regulatory protein asnC
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80.08.
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Best Local Similarity 80.09
Whiches 8, Conservative
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Best Local Similarity
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A:Molecule type: DNA
                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                            C;Accession: 097449
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Anathors: Postger, D. Fritz, C.; Philia, M.; Philia, Y.; Funa, S.; Salizzi, A.; Gallech, J.; Harwood, C.R.; Fritz, C.; Philia, M.; Philia, Y.; Funa, S.; Salizzi, A.; Gallech, J.; Harwood, C.R.; Prider, H.; Hoisappel, S.; Hosono, S.; Hulio, M. Keutler, P.; Romingstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A, Authors: Lauber, I. Lazarzvic, V.; Fee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maury, M.; Veyer, E. Harder, M.; Veyer, 
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Ayauthors: Ferreira, V.C.A.; Ferro, J.A.; Fraya, J.S.; Franca, S.C.; Franco, M.C.; Katalima, J.P.; Krieqer, J.E.; Kuramae, E.E.; Lachado, M.A.; Madelra, M.B.N.; Madelra, H.M.F.; Marino, C.L.; Marques, M.V.; Mattins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.N.; Miracca, E.C.; Miyaki, C.F.; Franco, M. W.; Madelra, M. W.; Menck, C.F.N.; Miracca, E.C.; Miyaki, C.F.; Franco, M. W.; Mara, M. W.; Madelli, R.V.; Sawa A.A.; Mara, A. J. de M.; de Kosa M.; V. P.; de Sa, P.G.; Santelli, R.V.; Sawa A.A.; M.H.; Vallada, M.; Van Sluys, M.A.; Verjovski-Almeida, S.; Veltore, A.L. A.Comtents: annotation
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A,Cross-references- GH-299114; GR-299115; GR-ALD09126; NID g2634478, PIPN.CAR12492.1;
A,Experimental source: strain 168
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Ajčross-relecences: EMBL:AF020713; NID:q3025478; FID:q3025571; FIDN:AAC13066.1
E.Kuist, F., Cassawati, N., Miszer, I., Albertini, A.M., Alberi, S., Arevedo, V.; Herring, R. Minn, S., Kreillini, S., Misselli, Y., Calidacii, H., Cagnator, V., Calider, N.M.; Minich, S.D., Emmerseo, F.I., Englan, K.E., Errington, J., Fabret, C.; Ferrari, Nature 390, 249-256, 1997
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A;Refarence number: A82515, MT:F.20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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C;Superfamily: Bacillus subtilis phage SPBc2 lypothetical protein yopW
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Length 321;

DB 2;

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R.Stover, C.K., Pham, X.Q., Erwin, A.L., Micoquelli, S.D.; Warrener, P.; Hickey, M.I.; adman, S.; Yuan, Y.; Brody, L.L., Coulter, S.N.; Folger, K.K.; Nas, A.; Larbiq, K.; L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                         Arītile: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
                                                                                                                                                                                                                                                                                                         A:Cross-references: GB:AE004744; GB:AE004091; NID:q9949417; PIDN:AAG06586.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rilln, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shon, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E, anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross references: GB:AE004054; GB:AE003849; NID:q9107645; PIDN:AAE85250.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.: Abreu, F.A.; Acencio, M.; Alvarenga, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis Udaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gross-references: GB: AFOGZOW4; NID: 94058480; PIDN: AAC98046.1; GSPDB: GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable adenylate kinase [imported] - Arabidopsis thaliana
CySpecies. Arabidopsis thaliana (mouse-ear eress)
CyEnter Ob-Peb-2001 #sequence_revision Op-Peb 2001 #text_change 02-Feb 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515: MUID:20365717; PMID:10910347
A:Note: Tor a complete list of authors see reference number A59328 below
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB 2; Length 250;
Pred. No. 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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                                                                                                                                                                   A;Reterence number: A82950; MUID:20437337; PMID:10984043
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HG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C
                                                                                                                                                                                                                                                                                                                                      A: Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                             65.58;
70.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.5%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 7. Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FLMLRLQDYE 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -284 <STO>
                                                                                                                                                                                                                                                                            1-250 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                         A; Status: preliminary
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                                                                                                                                                                                                                                                   A: Molecule type: DNA
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                                                                                                                                                                                               A; Accession: A83244
        C.Accession: A83244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: PA3198
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guery Match
                                                                                                                                                                                                                                                                            A, Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Title: The complete genome of the hyperthermophilic bacterium Aquitex aeolicus.
A; Reterence number: A70306. MITTE-WRINKER; FMID:95.47426
A; Arcession: A70364
A; Arcession: A70364
A; Stafus: preliminary: nucleic acid sequence not shown, translation not shown
A; Molecule type: DNA
A; Residuas: 1-37 - A0P.
A; Residuas: 1-37 - A0P.
A; Cross-reletences: GR-AP000705; GR-AE000657; NID:92983310; PIDN:AAC06914.1; PID:9298332
A; Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Presence of an extended duplication in the putative low-density-lipoprotein red
A;Reference number: IS1362; MUID:95324549; PMID:7541349
A;Accession: 865460
                                                                                                                                                                                                                                                                                                                                                                                   RiPeckert, G.: Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.E.; Graham, D.E.; Ov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein PA3198 limported] - Pseudomonas acruginosa (strain PAOI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Roywords: calcium, cholosterol motabolism; chylomicron; glycoprotein; intestine; LNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·.
                               ..
C:
                                                                                                                                                                                                                                                                                                C;Species: Aquitex aeolicus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2009)
C;Accession: A70364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Salmo salar (Atlantic salmon)
C.Dale: 04-Dec-1997 #sequepos_tryision 12 Dec-1997 #FeXt_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Speries: Pseudomonas aeruginosa
C.Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ačkosidučs: 17.1058 «Bab.
Azēross references: EMBLEXBIB56; NID:qB54519; PH.N.CAA57449 1; PH.GB54520
                                  Saps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47. DR 1: Length 337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                            2; Indels
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                                                                                                                                                                                                                                                                       conserved hypothetical protein aq_729 - Aquifex acolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Superfamily: conserved hypothetical protein MJ0674
                               2; Mismatches
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Pred. No. 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               apolipoprotein B - Atlantic salmon (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A:Residues: 1-1058 «BAB»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Habin, P.J.; Deryckere, F.; Gannon, F.
Enr. J. Biochem. 230, 45-51, 1995
63.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.88;
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                            7; Conservative
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Matches 7: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Accession: 865460; I51362
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  Best Local Similarity
                                                                                                                                   91 ELLIRIQPYAE 101
                                                                                1 BLMLRLODYER 11
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                         Matches
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A.A.A.Lors. Ferreira, V.C.A., Ferro, J.A., Flaga, J.S., Franca, S.C., Franco, M.C., Frohm J.D., Junquoira, M.L., Kemper, E.L., Kitajima, J.P., Kriqeer, J.E., Kuramae, E.E., Laign chado, M.A., Madelra, A.M.B.N., Madelra, H.M.F., Marins, E.E., Marques, M.V., Martins, E.A.A.Lifors. Martins, E.M.F., Malsukuma A.V., Menck, C.F.M.; Miracca, E.C., Miyaki, C.Y., F.G., Nunes, L.R., Oliveira, M.A., de Oliveira, M.C., de Oliveira, M.C., de Oliveira, M.C., Sahali, C.Y., Marthors: da Silva, A.C.K., de Silva, F.R., de Silva, A.M., Silva Jr., W.A., de Silva, R.M., Subhako, M.H., Vallada, H., Van Sluys, M.A., Verjovski Almeida, S., Vettore, A.L., A. A.C., Genetics: annotation
Briones, M.R.S.; Bueno, M.R.P.; Jamargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Has-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A: Cell Biol. 105, 843-853, 1987

A: Itle: Changes in the expression of alpha-fodrin during cabryonic development of Xenop A: Reference number: Soloul: MrID-87308.888; PMID-304.0772

A: Recession S01092

A: Molecule Lype: mRNA

A: Residues: 1-454 <GIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTOSS-references: EMBL:X06042; NID:g64700; PIDN:CAA29435.1; PID:g1334648
C:Supperfantly: Spectring alpha chain, calmodulin repeat homology; SB3 homology; spectring
C:Keywords: actin binding; EF hand
E:SidvyThamain: SpectringAstrephia repeat homology <SP6>
E:110-21/Chamain: SpectringAstrephia repeat homology <SP6>
E:110-21/Chamain: SpectringAstrephia repeat homology <SP7>
E:210-31/Chamain: SpectringAstrephia repeat homology; SP8>
E:407-454/Domain: SH3 homology <SH3>
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S01092
fourin alpha chain (clone alpha-2) - African clawed frog (fragment)
N'Altornate names: nonerythroid spectrin alpha chain
C'Species: Menopus laevis (African clawed frog)
C'Species: Wenopus laevis (African clawed frog)
C'Date: 01-Dec-1989 #sequence_rewision 01-Dec-1989 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0, Gaps
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